

OS Macadamia integrifolia.
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT /note="signal peptide"
 FT 29..666
 FT /note="mature protein"
 PN W09827805-A1.
 PD 02-JUL-1998.
 PF 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RTR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 DR N-PSDB: V42310.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 34-36; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 SV Sequence 666 AA;

Query Match 96.1%; Score 517; DB 1; Length 666;
 Best Local Similarity 95.7%; Pred. No. 2,29e-34;
 Matches 66; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 117 NRQDPQOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 176
 OY 117 NRQDPQOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 176

DB 177 ERMKEEDN 185
 OY 177 ERMKEEDN 185

RESULT 3
 ID W62830 standard; Protein; 625 AA.

AC W62830.
 DT 27-OCT-1998 (first entry)
 DE Macadamia integrifolia antimicrobial protein.
 KW Macadamia integrifolia; infestation; control.
 OS Macadamia integrifolia.
 FH Key Location/Qualifiers
 FT Peptide 1..28
 FT /note="signal peptide"
 FT 29..666
 FT /note="mature protein"
 PN W09827805-A1.
 PD 02-JUL-1998.
 PF 22-DEC-1997; AU0874.
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 PA (RTR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 DR N-PSDB: V42310.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 43-45; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 SV Sequence 625 AA;

Query Match 95.2%; Score 512; DB 1; Length 625;
 Best Local Similarity 94.2%; Pred. No. 6,11e-34;
 Matches 65; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 76 NRQDPQOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 135
 OY 117 NRQDPQOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 176
 DB 136 ERMKEEDN 144

OY 177 ERMKEEDN 185

RESULT 4
 ID W62831 standard; Protein; 525 AA.
 AC W62831.
 DT 27-OCT-1998 (first entry)
 DE Theobroma cacao antimicrobial protein.
 KW Antimicrobial protein; infestation; control.
 OS Theobroma cacao.
 PN W09827805-A1.
 PD 02-JUL-1998.
 PF 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RTR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-377279/32.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 PT useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 47-49; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 CC be used to control microbial infestations in plants and mammalian
 CC animals.
 SV Sequence 525 AA;

Query Match 40.9%; Score 220; DB 1; Length 525;
 Best Local Similarity 48.5%; Pred. No. 1.46e-09;
 Matches 32; Conservative 13; Mismatches 17; Indels 4; Gaps 3;

DB 35 ERDPQOYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 90
 OY 119 QRDPOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 178

DB 91 RQEQQ 96
 OY 179 RQEQQ 184

RESULT 5
 ID R20181 standard; Protein; 566 AA.

AC R20181.
 DT 16-APR-1992 (first entry)
 DE Sequence encoded by 67 kD T. cacao protein cDNA.
 KW Cocoa; Flavour; vicillin; seed storage protein.
 OS Theobroma cacao.
 PN W09119801-A.
 PD 26-DEC-1991.
 PR 07-JUN-1991; G00914.
 PR 11-JUN-1990; GB-013016.
 PA (MRS) MARS UK LTD.
 PI Spencer ME, Hodge R, Deakin EA, Ashton S;
 DR WPI: 92-024418/03.
 DR N-PSDB: 020377.
 PT Recombinant cocoa proteins - are responsible for flavour in cocoa
 PT beans and produced in large quantities using yeast and bacterial
 PT expression vectors
 PS Claim 4; Fig 2; 59pp; English.
 CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
 CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
 CC derived from the 67 kD precursor. T. cacao protein cDNA was
 CC detected in a cDNA library prepared from immature cocoa beans RNA
 CC using a probe based on the AA sequence of a CNBR peptide common to
 CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
 CC homologues between the 67 kD polypeptide and the vicillins, which are
 CC seed storage proteins.
 SV Sequence 566 AA;

Query Match 40.9%; Score 220; DB 1; Length 566;
 Best Local Similarity 48.5%; Pred. No. 1.46e-09;
 Matches 32; Conservative 13; Mismatches 17; Indels 4; Gaps 3;

DB 35 ERDPQOYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 90
 OY 119 QRDPOQYEQCQRRCRETEPRHMQTCQRCERREYERKROOKRYEQQREDEEKY 178

Qy	119	QRDPQOQYEQQECORHETPRHMQTCQNCERNEYEKRKQOKRIEQQREDEKXEE	178
Db	91	RCQEQQ	96
Qy	179	RMKEED	184

RESULT 6
ID W62832 standard; protein; 590 AA.
AC W62832:
DT 27-OCT-1998 (first entry)
DE Gossypium hirsutum antimicrobial protein.
DS antimicrobial protein; infestation; control.
OS Gossypium hirsutum.
PN WC9827805-A1.
PD 02-JUL-1998.
PE 22-DEC-1997.
PR 20-DEC-1996; AU-004275
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulier KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-317219/32.
PT Novel anti-microbial protein from e.g. *Macadamia integrifolia* -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 49-51: 96pp: English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 590 AA;

RESULT 7
ID W03340 standard: protein; 444 AA.
AC W03340;
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP1 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN W09853086-A1.
PD 26-NOV-1998.
PF 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD:
DR WPI: 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PT Claim 7; Page 36-37; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested
CC such as soybean). In contrast, decreased sucrose uptake activity in

cc seeds might be desirable where the vegetative material of the plant is
 cc harvested. The SBH regulatory regions confer specific or enhanced
 cc expression in developing seeds and so may be used to express any
 cc transgene in developing seeds.
 50 Sequence 444 AA;

[illegible]

RESULT	9
ID	w62835 standard; Protein: 593 AA.
AC	w62835;
DI	27-OCT-1998 (first entry)
DE	zea mays antimicrobial protein.
KW	antimicrobial protein; infestation; control.
OS	zea mays.
PN	W09827805-A1.
PD	02-JUL-1998.
PF	22-DEC-1997; AU0874.
PR	20-DEC-1996; AU-004275.
RA	(BETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.

CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 SQ Sequence 409 AA;

Query Match 19.9%; Score 107; DB 1; Length 409;
 Best Local Similarity 39.7%; Pred. No. 8.53e-01;
 Matches 23; Conservative 15; Mismatches 13; Indels 7; Gaps 4;
 DB 45 QCOO--QROYTES-DKRTCLQCCDSM--KQER--EKOVEETREKEEHOEHEDD 95
 QY 128 QCOERCOHETEPHMQTCQRCERREYERKQKQRYEBOQREDEKYEKREEDN 185

RESULT 14
 ID W90341 standard; protein: 489 AA.
 AC W90341;
 DT 24-MAY-1999 (first entry)
 DE G. max SBP2 protein.
 KM SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 OS Glycine max.
 PN M09853086-A1.
 PD 26-NOV-1998.
 PF 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 DR WPI: 99-070155/06.
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 PS Claim 13b; Page 37-38; SBP2; English.
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated
 CC from Glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 SQ Sequence 489 AA;

Query Match 19.9%; Score 107; DB 1; Length 489;
 Best Local Similarity 39.7%; Pred. No. 8.53e-01;
 Matches 23; Conservative 15; Mismatches 13; Indels 7; Gaps 4;

DB 45 QCOO--QROYTES-DKRTCLQCCDSM--KQER--EKOVEETREKEEHOEHEDD 95
 QY 128 QCOERCOHETEPHMQTCQRCERREYERKQKQRYEBOQREDEKYEKREEDN 185

RESULT 15
 ID W03474 standard; Protein: 395 AA.
 AC W03474;
 DT 23-OCT-1996 (first entry)
 DE Mouse SRY-related protein.

KW Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe;
 KM HMG box; human; bovine; sex; animal; birth.
 OS Mus musculus.
 PN J08154685-A.
 PD 18-JUN-1996.
 PF 30-NOV-1994; J19525.
 PR 30-NOV-1994; JP-319525.
 PA (KACH-) KACHIKU JUSEIRAN IISHOKU GIKUTSU KENKYUKU.
 DR WPI: 96-336575/34.
 N-PSDB: T33007.
 PT Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex
 PT of unborn animals
 PS Claim 1; Page 10-14; 21pp; Japanese.
 CC This is the amino acid sequence of a mouse SRY-related protein. The gene
 CC was isolated from a mouse genomic library using a cDNA fragment amplified
 CC by primers T33009-10 as a probe. The screen isolated 4 EcoRI fragments
 CC of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed
 CC a 240 bp HMG box sequence between bases 7154-7393. Similarity with the
 CC human SRY HMG box sequence resulted in primers being generated to amplify
 CC the human SRY HMG box sequence for use as a probe to isolate the bovine
 CC SRY-related gene (T33008). The mouse and bovine genes are useful for
 CC determining the sex of an animal prior to birth.
 SQ Sequence 395 AA;

Query Match 19.3%; Score 104; DB 1; Length 395;
 Best Local Similarity 16.9%; Pred. No. 1.41e+00;
 Matches 11; Conservative 11; Mismatches 20; Indels 3; Gaps 3;

DB 217 HHQOQOQFHDHQQOQOQOQOQFHDH--QK--QGFHDHQQOQOQFHDHQQOQOQFHD 273
 QY 119 QHDPQOQOQCOERCOHETEPHMQTCQRCERREYERKQKQRYEBOQREDEKYE 178
 DB 274 HQOQO 275
 QY 179 RMKEE 183

Search completed: Sat May 13 10:11:11 2000
 Job time : 8 secs.

